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FIG. 1A

```
   1  TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGGGGAGCC   60

  61  TCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGATAGGGCGAGGCT  120

 121  GTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGG  180
   1                                  M  A  S  S  I  L  K  W  V  V   10

 181  TCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGG  240
  11    S  H  Q  S  C  S  R  S  S  R  S  K  P  R  D  Q  R  E  E  A   30

 241  CCGGGAGCAGCGACCTGAGCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGG  300
  31    G  S  S  D  L  S  S  R  Q  D  A  E  N  A  E  A  K  L  R  G   50

 301  GCCTCCCGGGGCAGCTTGTGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGC  360
  51    L  P  G  Q  L  V  D  I  A  C  K  V  C  Q  A  Y  L  G  Q  L   70

 361  TGGAGCATGAGGACATCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGT  420
  71    E  H  E  D  I  D  T  S  A  D  A  V  E  D  L  T  E  A  E  W   90

 421  GGGAGGACCTGACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATT  480
  91    E  D  L  T  Q  Q  Y  Y  S  L  V  H  G  D  A  F  I  S  N  S  110

 481  CAAGAAATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC  540
 111    R  N  Y  F  S  Q  C  Q  A  L  L  N  R  I  T  S  V  N  P  Q  130

 541  AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGG  600
 131    T  D  I  D  G  L  R  N  I  W  I  I  K  P  A  A  K  S  R  G  150

 601  GCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACC  660
 151    R  D  I  V  C  M  D  R  V  E  E  I  L  E  L  A  A  A  D  H  170

 661  ACCCTCTTTCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCA  720
 171    P  L  S  R  D  N  K  W  V  V  Q  K  Y  I  E  T  P  L  L  I  190

 721  TCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGA  780
 191    C  D  T  K  F  D  I  R  Q  W  F  L  V  T  D  W  N  P  L  T  210

 781  CCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACA  840
 211    I  W  F  Y  K  E  S  Y  L  R  F  S  T  Q  R  F  S  L  D  K  230
```

**FIG. 1B**

```
841  AGCTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATG  900
231    L  D  S  A  I  H  L  C  N  N  A  V  Q  K  Y  L  K  N  D  V  250

901  TGGGCCGCAGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGT  960
251    G  R  S  P  L  L  P  A  H  N  M  W  T  S  T  R  F  Q  E  Y  270

961  ACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGA  1020
271    L  Q  R  Q  G  R  G  A  V  W  G  S  V  I  Y  P  S  M  K  K  290

1021 AGGCCATCGCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCT  1080
291    A  I  A  H  A  M  K  V  A  Q  D  H  V  E  P  R  K  N  S  F  310

1081 TTGAGCTCTACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGA  1140
311    E  L  Y  G  A  D  F  V  L  G  R  D  F  R  P  W  L  I  E  I  330

1141 TCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGG  1200
331    N  S  S  P  T  M  H  P  S  T  P  V  T  A  Q  L  C  A  Q  V  350

1201 TGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGC  1260
351    Q  E  D  T  I  K  V  A  V  D  R  S  C  D  I  G  N  F  E  L  370

1261 TCCTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGG  1320
371    L  W  R  Q  P  V  V  E  P  P  P  F  S  G  S  D  L  C  V  A  390

1321 CGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCT  1380
391    G  V  S  V  R  R  A  R  R  Q  V  L  P  V  C  N  L  K  A  S  410

1381 CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACC  1440
411    A  S  L  L  D  A  Q  P  L  K  A  R  G  P  S  A  M  P  D  P  430

1441 CTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGG  1500
431    A  Q  G  P  P  S  P  A  L  Q  R  D  L  G  L  K  E  E  K  G  450

1501 GGCTCCCCCTGGCCTTGCTGGCACCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCAC  1560
451    L  P  L  A  L  L  A  P  L  R  G  A  A  E  S  G  G  A  A  Q  470

1561 AGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACG  1620
471    P  T  R  T  K  A  A  G  K  V  E  L  P  A  C  P  C  R  H  V  490

1621 TGGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATC  1680
491    D  S  Q  A  P  N  T  G  V  P  V  A  Q  P  A  K  S  W  D  P  510
```

**FIG. 1C**

```
                .         .         .         .         .         .
1681  CAAACCAGCTAAATGCGCACCCGCTGGAGCCTGTGCTGCGGGGCCTGAAGACAGCAGAGG   1740
 511    N  Q  L  N  A  H  P  L  E  P  V  L  R  G  L  K  T  A  E  G   530

                .         .         .         .         .         .
1741  GCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCA   1800
 531    A  L  R  P  P  P  G  G  K  G  S                             541

                .         .         .
1801  GGAGTACAGGTTGCAGCCACTCTCCCAAGGGCGAATTC  1838
```

**FIG. 2**

```
                .         .         .         .         .         .
  1  ATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCCGAGAC   60
  1  I  D  G  L  R  N  I  W  I  I  K  P  A  A  K  S  R  G  R  D    20

                .         .         .         .         .         .
 61  ATAGTGTGCATGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTT   120
 21  I  V  C  M  D  R  V  E  E  I  L  E  L  A  A  A  D  H  P  L    40

                .         .         .         .         .         .
121  TCCAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGAC   180
 41  S  R  D  N  K  W  V  V  Q  K  Y  I  E  T  P  L  L  I  C  D    60

                .         .         .         .         .         .
181  ACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGG   240
 61  T  K  F  D  I  R  Q  W  F  L  V  T  D  W  N  P  L  T  I  W    80

                .         .         .         .         .         .
241  TTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGAC   300
 81  F  Y  K  E  S  Y  L  R  F  S  T  Q  R  F  S  L  D  K  L  D   100

                .         .         .         .         .         .
301  AGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGC   360
101  S  A  I  H  L  C  N  N  A  V  Q  K  Y  L  K  N  D  V  G  R   120

                .         .         .         .         .         .
361  AGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCTGCAG   420
121  S  P  L  L  P  A  H  N  M  W  T  S  T  R  F  Q  E  Y  L  Q   140

                .         .         .         .         .         .
421  CGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATC   480
141  R  Q  G  R  G  A  V  W  G  S  V  I  Y  P  S  M  K  K  A  I   160

                .         .         .         .         .         .
481  GCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTC   540
161  A  H  A  M  K  V  A  Q  D  H  V  E  P  R  K  N  S  F  E  L   180

                .         .         .         .         .         .
541  TACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCC   600
181  Y  G  A  D  F  V  L  G  R  D  F  R  P  W  L  I  E  I  N  S   200

                .         .         .         .         .         .
601  AGCCCCACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG   660
201  S  P  T  M  H  P  S  T  P  V  T  A  Q  L  C  A  Q  V  Q  E   220

                .         .         .         .         .         .
661  GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGG   720
221  D  T  I  K  V  A  V  D  R  S  C  D  I  G  N  F  E  L  L  W   240

721  AGGCAG  726
241  R  Q    242
```

**FIG. 3A**

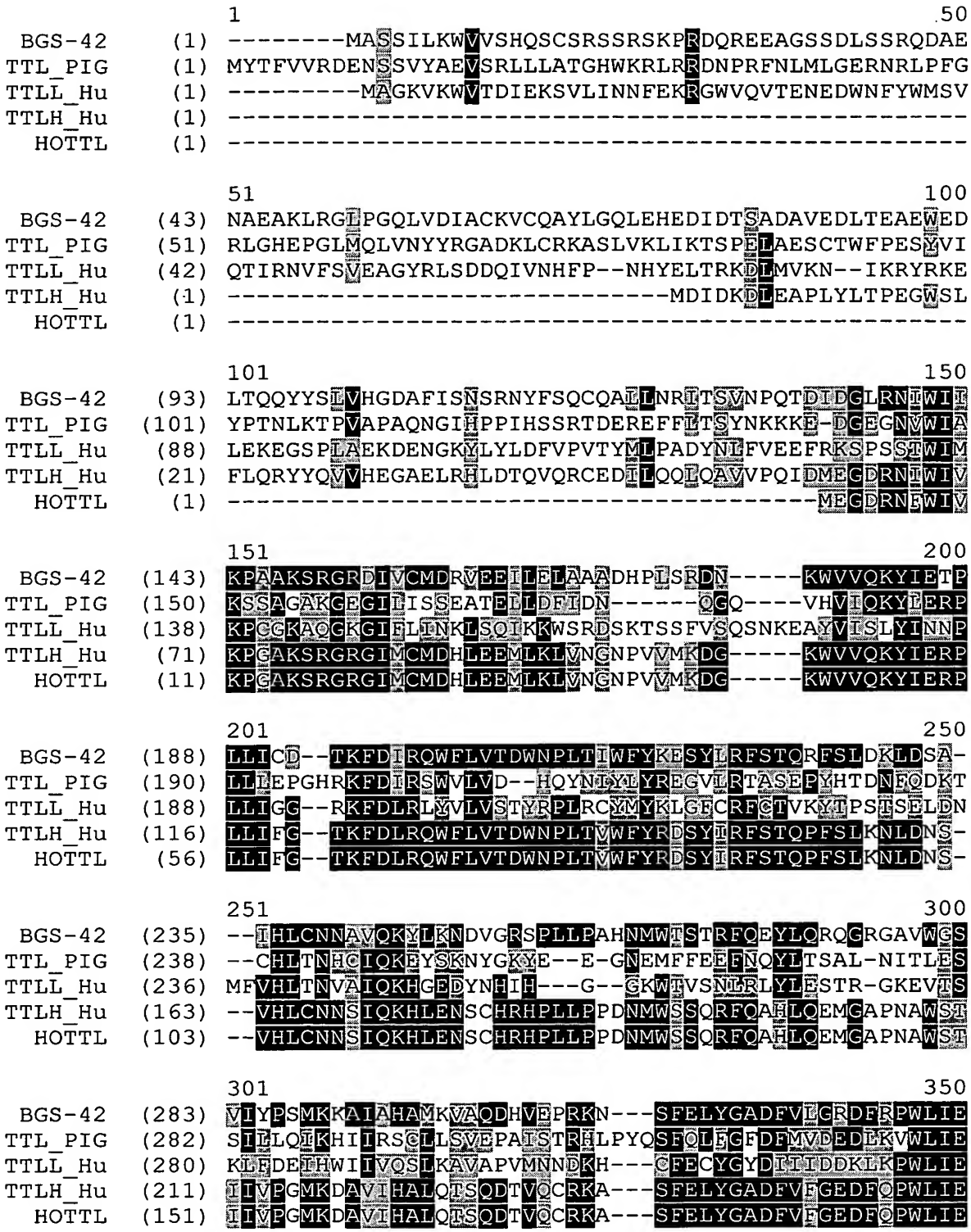
1 50
BGS-42 (1) --------MASSILKWVVSHQSCSRSSRSKPRDQREEAGSSDLSSRQDAE
TTL_PIG (1) MYTFVVRDENSSVYAEVSRLLLATGHWKRLRRDNPRFNLMLGERNRLPFG
TTLL_Hu (1) ---------MAGKVKWVTDIEKSVLINNFEKRGWVQVTENEDWNFYWMSV
TTLH_Hu (1) --------------------------------------------------
HOTTL (1) --------------------------------------------------
51 100
BGS-42 (43) NAEAKLRGLPGQLVDIACKVCQAYLGQLEHEDIDTSADAVEDLTEAEWED
TTL_PIG (51) RLGHEPGLMQLVNYYRGADKLCRKASLVKLIKTSPELAESCTWFPESYVI
TTLL_Hu (42) QTIRNVFSVEAGYRLSDDQIVNHFP--NHYELTRKDLMVKN--IKRYRKE
TTLH_Hu (1) ----------------------------MDIDKDLEAPLYLTPEGWSL
HOTTL (1) --------------------------------------------------
101 150
BGS-42 (93) LTQQYYSLVHGDAFISNSRNYFSQCQALLNRLTSVNPQTDIDGLRNIWII
TTL_PIG (101) YPTNLKTPVAPAQNGIHPPIHSSRTDEREFFLTSYNKKKE-DGEGNVWIA
TTLL_Hu (88) LEKEGSPLAEKDENGKYLYLDFVPVTYMLPADYNLFVEEFRKSPSSTWIM
TTLH_Hu (21) FLQRYYQVVHEGAELRHLDTQVQRCEDILQQLQAVVPQIDMEGDRNIWIV
HOTTL (1) ----------------------------------------MEGDRNFWIV
151 200
BGS-42 (143) KPAAKSRGRDIVCMDRVEEILELAAADHPLSRDN-----KWVVQKYIETP
TTL_PIG (150) KSSAGAKGEGILISSEATELLDFIDN------QGQ----VHVIQKYIERP
TTLL_Hu (138) KPCGKAQGKGIFLINKLSQIKKWSRDSKTSSFVSQSNKEAYVISLYINNP
TTLH_Hu (71) KPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDG-----KWVVQKYIERP
HOTTL (11) KPGAKSRGRGIMCMDHLEEMLKLVNGNPVVMKDG-----KWVVQKYIERP
201 250
BGS-42 (188) LLICD--TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFSLDKLDSA-
TTL_PIG (190) LLLEPGHRKFDIRSWVLVD--HQYNIYLYREGVLRTASEPYHTDNEQDKT
TTLL_Hu (188) LLIGG--RKFDLRLYVLVSTYRPLRCYMYKLGFCRFGTVKYTPSTSELDN
TTLH_Hu (116) LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-
HOTTL (56) LLIFG--TKFDLRQWFLVTDWNPLTVWFYRDSYIRFSTQPFSLKNLDNS-
251 300
BGS-42 (235) --IHLCNNAVQKYLKNDVGRSPLLPAHNMWISTRFQEYLQRQGRGAVWGS
TTL_PIG (238) --CHLTNHCIQKEYSKNYGKYE--E-GNEMFFEEFNQYLTSAL-NITLES
TTLL_Hu (236) MFVHLTNVAIQKHGEDYNHIH---G--GKWTVSNLRLYLESTR-GKEVTS
TTLH_Hu (163) --VHLCNNSIQKHLENSCHRHPLLPPDNMWSSQRFQAHLQEMGAPNAWST
HOTTL (103) --VHLCNNSIQKHLENSCHRHPLLPPDNMWSSQRFQAHLQEMGAPNAWST
301 350
BGS-42 (283) VIYPSMKKAIAHAMKVAQDHVEPRKN---SFELYGADFVLGRDFRPWLIE
TTL_PIG (282) SILLQIKHIIRSCLLSVEPAISTRHLPYQSFQLEGFDFMVDEDLKVWLIE
TTLL_Hu (280) KLFDEIHWIIVQSLKAVAPVMNNDKH---CFECYGYDIIIDDKLKPWLIE
TTLH_Hu (211) IIVPGMKDAVIHALQTSQDTVQCRKA---SFELYGADFVFGEDFQPWLIE
HOTTL (151) IIVPGMKDAVIHALQTSQDTVQCRKA---SFELYGADFVFGEDFQPWLIE

**FIG. 3B**

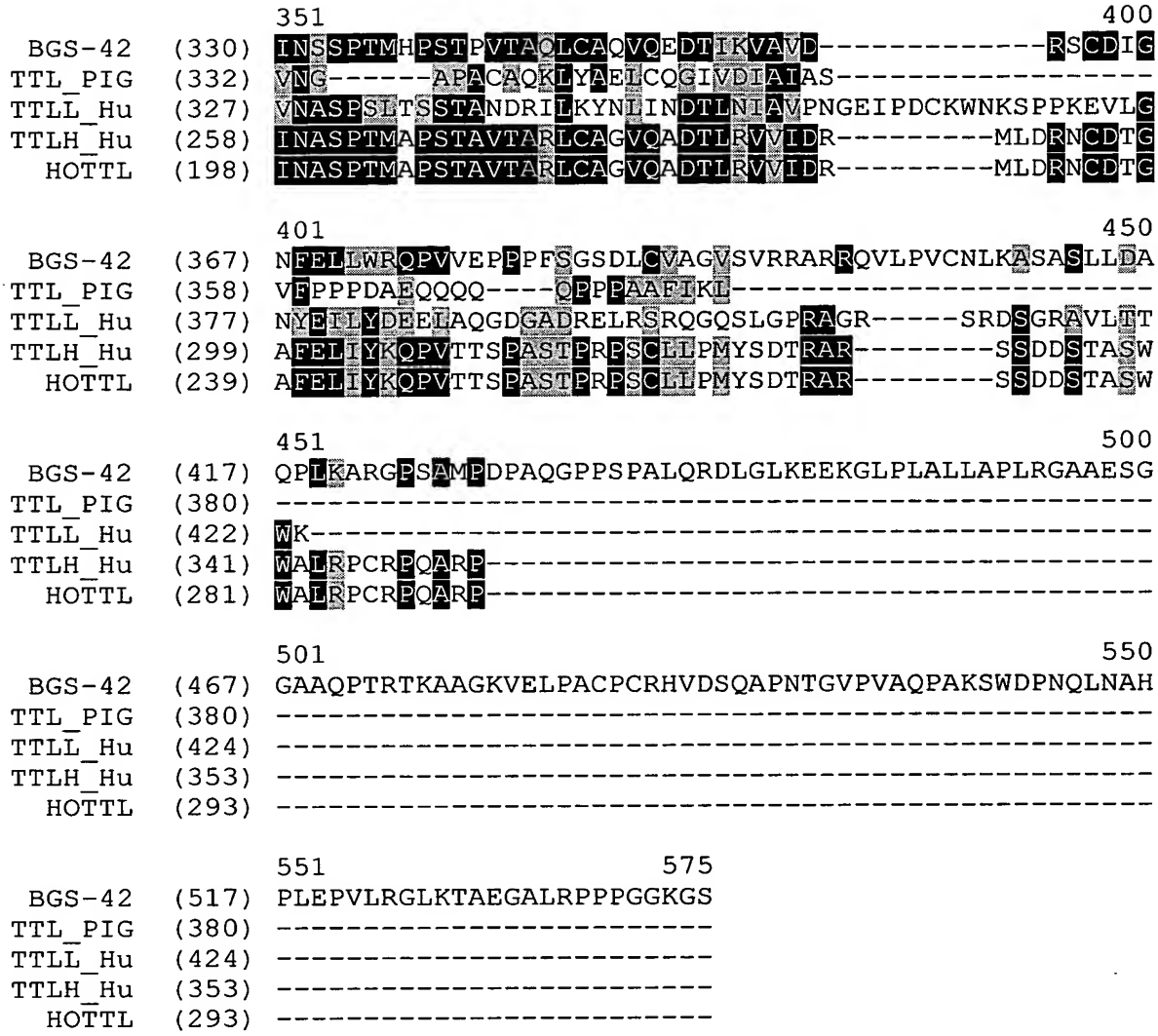
351 400
BGS-42 (330) INSSPTMHPSTPVTAQLCAQVQEDTIKVAVD----------RSCDIG
TTL_PIG (332) VNG------APACAQKLYAELCQGIVDIAIAS----------
TTLL_Hu (327) VNASPSLTSSTANDRILKYNLINDTLNIAVPNGEIPDCKWNKSPPKEVLG
TTLH_Hu (258) INASPTMAPSTAVTARLCAGVQADTLRVVIDR---------MLDRNCDTG
HOTTL (198) INASPTMAPSTAVTARLCAGVQADTLRVVIDR---------MLDRNCDTG
401 450
BGS-42 (367) NFELLWRQPVVEPPPFSGSDLCVAGVSVRRARRQVLPVCNLKASASLLDA
TTL_PIG (358) VFPPPDAEQQQQ----QPPPAAFIKL----------
TTLL_Hu (377) NYEILYDEELAQGDGADRELRSRQGQSLGPRAGR-----SRDSGRAVLTT
TTLH_Hu (299) AFELIYKQPVTTSPASTPRPSCLLPMYSDTRAR--------SSDDSTASW
HOTTL (239) AFELIYKQPVTTSPASTPRPSCLLPMYSDTRAR--------SSDDSTASW
451 500
BGS-42 (417) QPLKARGPSAMPDPAQGPPSPALQRDLGLKEEKGLPLALLAPLRGAAESG
TTL_PIG (380) ----------
TTLL_Hu (422) WK----------
TTLH_Hu (341) WALRPCRPQARP----------
HOTTL (281) WALRPCRPQARP----------
501 550
BGS-42 (467) GAAQPTRTKAAGKVELPACPCRHVDSQAPNTGVPVAQPAKSWDPNQLNAH
TTL_PIG (380) ----------
TTLL_Hu (424) ----------
TTLH_Hu (353) ----------
HOTTL (293) ----------
551 575
BGS-42 (517) PLEPVLRGLKTAEGALRPPPGGKGS
TTL_PIG (380) ----------
TTLL_Hu (424) ----------
TTLH_Hu (353) ----------
HOTTL (293) ----------

**FIG. 4**

| Model | Description | Score | E-value | N |
|---|---|---|---|---|
| TTL | Tubulin-tyrosine ligase family | 293.0 | 3.7e-84 | 1 |

```
Q       73 EDIDTS----ADAVEDLTEAEWEDLTQQYYSLVHGDAFISNSR-------NYFSQCQALL
           ++ID +     +++ ++ +  W   ++ ++  ++  + +             ++  +++++
T        1 MRIDMHYRMMHQMINHFPGSYWITRKDRLWMNIKRMMCDFHWKHDHFDWMPRTFILPTDY

Q      122 NRITSVNPQTDIDGLRNIWIIKPAAKSRGRDIVCMDRVEEILELAA-----ADHPLSRDN
           +++ +  ++ + +G++N+WI+KP++++RGR+I++M+  ++I+ ++          +P++ ++
T       61 QEFVDYWQKHEWWGQDNHWIVKPWNSCRGRGIWIMNDWKQIPRWVNDFMDNPFVPQHQRR

Q      177 KWVVQKYIETPLLICD-----TKFDIRQWFLVTDWNPLTIWFYKESYLRFSTQRFS--LD
           +WVVQKYIE PLLI        +KFDIR+++LVT++NPL+I++Y+E+++RF+++ ++    +
T      121 PWVVQKYIERPLLIDGMDVGHHKFDIRCYVLVTSFNPLRIYVYREGWCRFCSVKYHPMDN

Q      230 KLDSAIHLCNNAVQKYLKN--DVGRSPLLPAHNMWTSTRFQEYLQR--QGRGAVWGSVIY
             +  +HL+N+++QK+ +N     +R ++++ ++MWT  +F++Y+++    +  ++W +++
T      181 FDNYCMHLTNYCIQKHYSNYSRCNRDYNECHGHMWTLQNFWNYYENMGIDWDNIWSQICD

Q      286 PSMKKAIAHA-MKVAQDHVEPRKNSFELYGADFVL----GRDFRPWLIEINSSPTMHPST
           + +K+++A++ +++++++++PR+N+FELYG+DF +      +++ PWL+E+N+SP+MH+++
T      241 IIIKTIVAAWCVEACRMNMQPRYNCFELYGFDFMIQWDDDENLKPWLLEVNWSPDMHCTC

Q      341 PVTAQLCAQVQEDTIK-----VAVDRSCDI
           P+++ LC+Q+++D+++      V +D++ D+
T      301 PYDMHLCHQLIRDVLNCAGCHVPPDCMKDC
```

FIG. 5A

**BGS-42 – Clone A**

TGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGTTGG
GGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGAT
AGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCCAGC
ATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGCAAG
CCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCAAGA
TGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGACAT
CGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCGA
CACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGAC
CCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATT
ACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGAC
GGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCG
GGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTC
ATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGGAACC
CCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGCGCTT
CTCCCTGGACAAGCTGGACAGCGCCATCCACCTGTGCAACAACACCGTCCAGAA
GTACCTGAAGAATGATGTGGGCCGCAGCCCCCTGCTGCCCGCACACAACATGTG
GACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTG
GGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCATGAAGGT
GGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGA
CTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCC
ACCATGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAG
GACACCATCAAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTC
CTGTGGAGGCAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCG
TGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACC
TCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCT
CGGCCATGCCAGACCCTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTT
GGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCTTAAGGGG
GGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAA
GGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAAACAC
CGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGA
GCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCG
TCCGCCGCCCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAG
TACAGGTTGCAGCCACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGT
CTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAG
CTGTCAGTTCTATCTGCCAGCTTTTGAGTGTTCAATTTGATTTTTACTTATTCAACC
TGGAATTTGAATGTCAAAAAAAAAAAAAAAAAAA (SEQ ID NO:9)

**FIG. 5B**

**BGS-42 – Clone B**

GTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAGACTTCCGGCGCACCATGGCATC
CAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAG
CAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGC
AAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGG
ACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACA
TCGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACC
TGACCCAGCAGTACTACTCCCTCGTTCATGCCAGGCTCTGCTGAATAGAATCACG
TCTGTGAACCCTCAGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGC
CCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCATGGACCGTGTGGAGGAGA
TCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACAACAAGTGGGTGGT
CCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCGACATCAG
ACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAGGAG
AGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCA
TCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCA
GCCCCCTGCTGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCT
GCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAA
GAAGGCCATCGCCCACGCCATGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAA
GAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTTGGGAGGGACTTCAGGCCC
TGGCTGATCGAGATCAATTCCAGCCCCACCATGCACCCGTCCACGCCGGTCACGG
CCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCAAGGTGGCCGTGGACCGCA
GCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGCCGGTGGTTGAGCCGCCCCCA
TTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGAGAGCCAGGAGG
CAGGTGCTGCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACGCGCAGC
CGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCCAT
CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGG
CCTTGCTGGCACCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCA
CCCGCACCAAAGCTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGT
GGACAGTCAGGCCCCAAACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTG
GGATCCAAACCAGCTAAATGAGCACCCGCTGGAGCCTGTGCTGCGGAGCCTGAA
GACAGCAGAGGGCGCGCTGCGTCCGCCGCCCGGAGGAAAAGGTTCATGACAGCG
TCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCCACTCTCCCGCCGAACATTGA
ATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGGAAAATCAGCAGAGTC
AGCCATCACTCTCCAAGGGGAGCTGTCAGTTCTATCTGCCAGCTTTTGAGTGTTC
AATTTGATTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAAAAAAAA
AAAAAAAAA (SEQ ID NO:10)

FIG. 5C

**BGS-42 – Clone C**

CCCAGGACTCCTGGTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCCACCC
CCAGCACCCCTGTGCCCTTTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAA
GCTCCCTCCTCAGGGCACAGAGGCCAAAGATGGGGCTGACTGGGGGCTGCCACC
GGGCTTTGGGTGCTGAGGGGGCTGTGGGACCCCAGGGGAAGAGGTGCCGCTCCC
CCCAGCACCGGGCACTCCCCCGCCTCCCCCGGCCTCCAGCCCTGCACAAAGCAGC
TTGCCACACCCTTCCCACCAAGGCCCAGGGCTGAGGCCTGCCCAGGACGCAGGG
TGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGGCTTCCCTGGCACAGA
GGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAGGT
GCAGGACAAGGTTCCCTTCCGCACCTAATACCCCAGGGTCAGGCCAGCGCCAGC
GCTGCTAGTGGCAACATGGCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGC
GTGCGCTGTGTTTTCTGGGGGCCAGCCACTTTTTTCCTTAACGGGGTGACAAACC
AGACATCGGGGTGCGGGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCT
CGCGTGTGGTGGGCAGTGCTGGGCATGTGGCTGCGTTCCGGGCCCTGCAGCCGCT
CCTCCCTCTCCTGGGGTCTGAGGTGTGGGACACCCTGTGGCCCGTTTGGGGGCCT
GGAGGGAGCCCCAGTGCCCACCGCCCTCGGTGCCCTCAGCTGCAGCCTCCCCATT
CCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGGATGCGTCTGAGCCTGGCCTG
CACATCCATGCTCCCACCGGCTGGAGGGGGTGTTCTGGGGCCCTGGGGGACCGT
ATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTGCCCCATAG
CCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAGCT
GAGCTGAGCTGCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTG
CGTGAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTTC
CCACGCTGCTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAG
TGAGGAGACGGCAGAGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGAT
CCCCCTGGTGCTGAGACAGACTGATGGGGCAGGGTCTGAGGATAGAGGACCGGG
GAGAGGCCTCCCATGGTCATGGTCATGGCAGTACAGAGGCCAGGGGCCCCGGGA
GGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTCTGTGCTAGGCTTGTGGACAGCG
CGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTCGGAGGCCGAGGGGTGCAGC
TGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGCAGACTGGGG
GTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCGGGT
TGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACA
GATAGGGCGAGGCTGTGCTGTCCTTTCAGAAGACTTCCGGCGCACCATGGCATCC
AGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCAGCAGGAGCAGCAGAAGC
AAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGAGCAGCAGGCA
AGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTGTGGA
CATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACAT
CGACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCT
GACCCAGCAGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGA
AATTACTTTTCGCAGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTC
AGACGGACATTGACGGGCTCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGT
CCCGGGGCCGAGGGACAACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCT
GCTCATCTGTGACACCAAGTTCGACATCAGACAGTGGTTCCTCGTCACGGACTGG
AACCCCCTGACCATCTGGTTCTACAAGGAGAGTTACTTGCGGTTCTCAACTCAGC
GCTTCTCCCTGGACAAG

**FIG. 5C (CONT.)**

CTGGACAGCGCCATCCACCTGTGCAACAACGCCGTCCAGAAGTACCTGAA
GAATGATGTGGGCCGCAGCCCCCTGCTGCCCGCACACAACATGTGGACCAGCAC
CAGGTTCCAGGAGTACCTGCAGCGCCAGGGCCGTGGCGCCGTGTGGGGCAGCGT
CATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCATGAAGGTGGCCCAGGA
CCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTGACTTCGTCCTT
GGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCATGCAC
CCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATC
AAGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGG
CAGCCGGTGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGGCGGGCG
TCAGTGTGAGGAGAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCT
CGGCCTCGCTGTTGGACGCGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGC
CAGACCCTGCCCAGGGACCCCCATCACCAGCTCTCCAGCGGGACTTGGGACTGA
AGGAAGAGAAGGGGCTCCCCCTGGCCTTGCTGGCACCCTTAAGGGGGGCAGCCG
AGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAGCTGCTGGGAAGGTGGAGC
TCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAAACACCGGTGTCCC
CGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGCACCCGCT
GGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGCC
CGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTG
CAGCCACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGT
GGCTCTGGGAAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGT
TCTATCTGCCAGCTTTTGAGTGTTCAATTTGATTTTTACTTATTCAACCTGGAATTT
GAATGTCAAAAAAAAAAAAAAAAAAAA (SEQ ID NO:11)

**FIG. 6A**

```
   1  GTCTAAGGCCGTGGCCAGAATCACTCGGTGCCCACCCCACCCCCAGCACCCCTGTGCCCT   60

  61  TTGCTCTGTGTCTCTGGGTGAATCCGGGGCCCCAGAAGCTCCCTCCTCAGGGCACAGAGG  120

 121  CCAAAGATGGGGCTGACTGGGGGCTGCCACCGGGCTTTGGGTGCTGAGGGGGCTGTGGGA  180

 181  CCCCAGGGGAAGAGGTGCCGCTCCCCCCAGCACCGGGCACTCCCCCGCCTCCCCCGGCCT  240

 241  CCAGCCCTGCACAAAGCAGCTTGCCACACCCTTCCCACCAAGGCCCAGGGCTGAGGCCTG  300

 301  CCCAGGACGCAGGGTGTGGGGACCCTGCTGAGGGAGGGGTCCCGGAAGAGGGGCTTCCCT  360

 361  GGCACAGAGGTCCCTCTCAGCAGGCCAGGTGCGGCTGCCTCAGCACAGTGTGGGGCGGAG  420

 421  GTGCAGGACAAGGTTCCCTTCCGCACCTAATACCCCAGGGTCAGGCCAGCGCCAGCGCTG  480

 481  CTAGTGGCAACATGGCCCCTTCAAAGACCCCGTGTGCAGAGCCAGTCAGCGTGCGCTGTG  540

 541  TTTTCTGGGGGCCAGCCACTTTTTTCCTTAACGGGGTGACAAACCAGACATCGGGGTGCG  600

 601  GGGACTTCACGATATGCCTCTCTAATGGCGCGTGCTACCTCGCGTGTGGTGGGCAGTGCT  660

 661  GGGCATGTGGCTGCGTTCCGGGCCCTGCAGCCGCTCCTCCCTCTCCTGGGGTCTGAGGTG  720

 721  TGGGACACCCTGTGGCCCGTTTGGGGGCCTGGAGGGAGCCCCAGTGCCCACCGCCCTCGG  780

 781  TGCCCTCAGCTGCAGCCTCCCCATTCCCTGGGGCCTGCCACGCCCTCCACTGCCTCAAGG  840

 841  ATGCGTCTGAGCCTGGCCTGCACATCCATGCTCCCACCGGCTGGAGGGGGTGTTCTGGGG  900

 901  CCCTGGGGGACCGTATATCTGGGGAGGGGGAGGGATCCGCCCTAGGGGTGCTGTGTGGTG  960

 961  CCCCATAGCCAGGCAAGTCTGAGGTGGACGGCCCGTCCTCGCCTTGTGAGCGAGGCAGAG 1020

1021  CTGAGCTGAGCTGCCCCTCCTGCCTAACACGCCACTGTCTCTGGAGATCGGGCTGTGCGT 1080

1081  GAACATGCGGAGCCTGCCCTGGTACGTCCCGGCCAACCCCGACTCCTTCTTCCCACGCTG 1140
```

**FIG. 6B**

```
1141  CTACAGCCTCTGCACCGAGAGTGAGCAGCAGGAGTTCCTGGGTAAGTGAGGAGACGGCAG  1200

1201  AGGGCCCCAGTGCTGTCAGCAGAGAGGCTTCTAGAAAGATCCCCCTGGTGCTGAGACAGA  1260

1261  CTGATGGGGCAGGGTCTGAGGATAGAGGACCGGGGAGAGGCCTCCCATGGTCATGGTCAT  1320

1321  GGCAGTACAGAGGCCAGGGGCCCCGGGAGGGAGGGCGGGCAGTCAAGGAGTGTGTGGTTC  1380

1381  TGTGCTAGGCTTGTGGACAGCGCGGCGAGCAGCTGGGGCAAGGCCGGCTCCGTGGTCGGA  1440

1441  GGCCGAGGGGTGCAGCTGGACGGCCGCAGTCACAGAGACACTGCAGGGAGAAGGGCAGGC  1500

1501  AGACTGGGGGTGTGGGAGCAGGCCTGGGCCCCATCGGCTATGAGGGCGGGAAGTGGGGCG  1560

1561  GGTTGGGGAGCCTCCGTGGCCCTGGCCCCATCTCCAGTCCCCAGTCCTGGCTCGGACAGA  1620

1621  TAGGGCGAGGCTGTGCTGTCCTTTCAGAGTAGCAGCGTGGGAAGAAGGAGTTCCTGGAAG  1680

1681  ACTTCCGGCGCACCATGGCATCCAGCATCCTCAAGTGGGTGGTCAGCCACCAGAGCTGCA  1740
   1                M  A  S  S  I  L  K  W  V  V  S  H  Q  S  C  S   16

1741  GCAGGAGCAGCAGAAGCAAGCCCAGGGACCAGAGGGAGGAGGCCGGGAGCAGCGACCTGA  1800
  17    R  S  S  R  S  K  P  R  D  Q  R  E  E  A  G  S  S  D  L  S   36

1801  GCAGCAGGCAAGATGCTGAAAATGCTGAGGCAAAGCTCAGGGGCCTCCCGGGGCAGCTTG  1860
  37    S  R  Q  D  A  E  N  A  E  A  K  L  R  G  L  P  G  Q  L  V   56

1861  TGGACATCGCGTGCAAGGTGTGCCAGGCCTACCTGGGGCAGCTGGAGCATGAGGACATCG  1920
  57    D  I  A  C  K  V  C  Q  A  Y  L  G  Q  L  E  H  E  D  I  D   76

1921  ACACGTCAGCAGATGCCGTGGAGGACCTCACTGAGGCCGAGTGGGAGGACCTGACCCAGC  1980
  77    T  S  A  D  A  V  E  D  L  T  E  A  E  W  E  D  L  T  Q  Q   96

1981  AGTACTACTCCCTCGTTCATGGCGATGCTTTCATCTCCAATTCAAGAAATTACTTTTCGC  2040
  97    Y  Y  S  L  V  H  G  D  A  F  I  S  N  S  R  N  Y  F  S  Q  116

2041  AGTGCCAGGCTCTGCTGAATAGAATCACGTCTGTGAACCCTCAGACGGACATTGACGGGC  2100
 117    C  Q  A  L  L  N  R  I  T  S  V  N  P  Q  T  D  I  D  G  L  136
```

FIG. 6C

```
2101  TCCGGAACATCTGGATTATAAAGCCCGCGGCCAAGTCCCGGGGCCGAGACATAGTGTGCA  2160
 137    R  N  I  W  I  I  K  P  A  A  K  S  R  G  R  D  I  V  C  M   156

2161  TGGACCGTGTGGAGGAGATCCTGGAGCTGGCAGCTGCAGACCACCCTCTTTCCAGGGACA  2220
 157    D  R  V  E  E  I  L  E  L  A  A  A  D  H  P  L  S  R  D  N   176

2221  ACAAGTGGGTGGTCCAGAAGTACATCGAGACGCCGCTGCTCATCTGTGACACCAAGTTCG  2280
 177    K  W  V  V  Q  K  Y  I  E  T  P  L  L  I  C  D  T  K  F  D   196

2281  ACATCAGACAGTGGTTCCTCGTCACGGACTGGAACCCCCTGACCATCTGGTTCTACAAGG  2340
 197    I  R  Q  W  F  L  V  T  D  W  N  P  L  T  I  W  F  Y  K  E   216

2341  AGAGTTACTTGCGGTTCTCAACTCAGCGCTTCTCCCTGGACAAGCTGGACAGCGCCATCC  2400
 217    S  Y  L  R  F  S  T  Q  R  F  S  L  D  K  L  D  S  A  I  H   236

2401  ACCTGTGCAACAACGCCGTCCAGAAGTACCTGAAGAATGATGTGGGCCGCAGCCCCCTGC  2460
 237    L  C  N  N  A  V  Q  K  Y  L  K  N  D  V  G  R  S  P  L  L   256

2461  TGCCCGCACACAACATGTGGACCAGCACCAGGTTCCAGGAGTACCTGCAGCGCCAGGGCC  2520
 257    P  A  H  N  M  W  T  S  T  R  F  Q  E  Y  L  Q  R  Q  G  R   276

2521  GTGGCGCCGTGTGGGGCAGCGTCATCTACCCGTCCATGAAGAAGGCCATCGCCCACGCCA  2580
 277    G  A  V  W  G  S  V  I  Y  P  S  M  K  K  A  I  A  H  A  M   296

2581  TGAAGGTGGCCCAGGACCACGTGGAGCCTCGCAAGAACAGCTTTGAGCTCTACGGGGCTG  2640
 297    K  V  A  Q  D  H  V  E  P  R  K  N  S  F  E  L  Y  G  A  D   316

2641  ACTTCGTCCTTGGGAGGGACTTCAGGCCCTGGCTGATCGAGATCAATTCCAGCCCCACCA  2700
 317    F  V  L  G  R  D  F  R  P  W  L  I  E  I  N  S  S  P  T  M   336

2701  TGCACCCGTCCACGCCGGTCACGGCCCAGCTGTGTGCACAGGTGCAGGAGGACACCATCA  2760
 337    H  P  S  T  P  V  T  A  Q  L  C  A  Q  V  Q  E  D  T  I  K   356

2761  AGGTGGCCGTGGACCGCAGCTGTGACATCGGCAACTTCGAGCTCCTGTGGAGGCAGCCGG  2820
 357    V  A  V  D  R  S  C  D  I  G  N  F  E  L  L  W  R  Q  P  V   376

2821  TGGTTGAGCCGCCCCCATTCAGCGGGTCCGACCTCTGCGTGGCGGGCGTCAGTGTGAGGA  2880
 377    V  E  P  P  P  P  F  S  G  S  D  L  C  V  A  G  V  S  V  R  R   396

2881  GAGCCAGGAGGCAGGTGCTGCCCGTCTGCAACCTCAAGGCCTCGGCCTCGCTGTTGGACG  2940
 397    A  R  R  Q  V  L  P  V  C  N  L  K  A  S  A  S  L  L  D  A   416
```

**FIG. 6D**

```
2941  CGCAGCCGCTGAAGGCACGGGGCCCCTCGGCCATGCCAGACCCTGCCCAGGGACCCCCAT  3000
 417    Q  P  L  K  A  R  G  P  S  A  M  P  D  P  A  Q  G  P  P  S   436

3001  CACCAGCTCTCCAGCGGGACTTGGGACTGAAGGAAGAGAAGGGGCTCCCCCTGGCCTTGC  3060
 437    P  A  L  Q  R  D  L  G  L  K  E  E  K  G  L  P  L  A  L  L   456

3061  TGGCACCCTTAAGGGGGGCAGCCGAGAGCGGTGGAGCCGCACAGCCCACCCGCACCAAAG  3120
 457    A  P  L  R  G  A  A  E  S  G  G  A  A  Q  P  T  R  T  K  A   476

3121  CTGCTGGGAAGGTGGAGCTCCCGGCCTGCCCCTGTCGCCACGTGGACAGTCAGGCCCCAA  3180
 477    A  G  K  V  E  L  P  A  C  P  C  R  H  V  D  S  Q  A  P  N   496

3181  ACACCGGTGTCCCCGTAGCCCAGCCCGCCAAAAGCTGGGATCCAAACCAGCTAAATGAGC  3240
 497    T  G  V  P  V  A  Q  P  A  K  S  W  D  P  N  Q  L  N  E  H   516

3241  ACCCGCTGGAGCCTGTGCTGCGGAGCCTGAAGACAGCAGAGGGCGCGCTGCGTCCGCCGC  3300
 517    P  L  E  P  V  L  R  S  L  K  T  A  E  G  A  L  R  P  P  P   536

3301  CCGGAGGAAAAGGTTCATGACAGCGTCAGATTCTCTGCAGCAGGAGTACAGGTTGCAGCC  3360
 537    G  G  K  G  S                                               541

3361  ACTCTCCCGCCGAACATTGAATACGTCTTTCCACCATCTTGTCTTTGCTGTGGCTCTGGG  3420

3421  AAAATCAGCAGAGTCAGCCATCACTCTCCAAGGGGAGCTGTCAGTTCTATCTGCCAGCTT  3480

3481  TTGAGTGTTCAATTTGATTTTTACTTATTCAACCTGGAATTTGAATGTCAAAAAAAAAAA  3540

3541  AAAAAAAAAAAAAA  3554
```

FIG. 7A

-2057 tgcctgcagcagagcccggctgggatcctcacgctgcacgccatttgtcctctgatggtt -1998

-1997 gcctcactccatcccatcctggctggtgtgaaccttgaatgctgggcatcaataaagact -1938

-1937 tttttcttgccagtctaggttggtaaaaaatgagatgccgtacctcctctggaccatcaa -1878

-1877 gagggacatcattgactatcacagcctgacctacgaccagatgctgaaccactacgcaaa -1818

-1817 gacagcctccttcaccaccaaggtgagccggccgcgcttgagcgtggcgggagccggcaa -1758

-1757 gggtggtggggaggagcttctgcagccattagggaccctcggtggctggtcagtggccac -1698

-1697 cagtcacctcctgggtgcatcccaggactcctggtctaaggccgtggccagaatcactcg -1638

-1637 gtgcccaccccaccccagcacccctgtgcccttgctctgtgtctctgggtgaatccgg -1578

-1577 ggccccagaagctccctcctcagggcacagaggccaaagatggggctgactgggggctgc -1518

-1517 caccgggctttgggtgctgaggggctgtgggaccccaggggaagaggtgccgctccccc -1458

-1457 cagcaccgggcactcccccgcctcccccggcctccagccctgcacaaagcagcttgccac -1398

-1397 acccttcccaccaaggcccagggctgaggcctgcccaggacgcagggtgtggggaccctg -1338

-1337 ctgagggaggggtcccggaagaggggcttccctggcacagaggtccctctcagcaggcca -1278

-1277 ggtgcggctgcctcagcacagtgtggggcggaggtgcaggacaaggttcccttccgcacc -1218

-1217 taataccccagggtcaggccagcgccagcgctgctagtggcaacatggccccttcaaaga -1158

-1157 ccccgtgtgcagagccagtcagcgtgcgctgtgttttctgggggccagccacttttttcc -1098

-1097 ttaacagggtgacaaaccagacatcggggtgcggggacttcacgatatgcctctctaatg -1038

-1037 gcgcgtgctacctcgcgtgtggtgggcagtgctgggcatgtggctgcgttccgggccctg -978

-977 cagccgctcctccctctcctggggtctgaggtgtgggacaccctgtggcccgtttggggg -918

-917 cctggagggagccccagtgcccaccgccctcggtgccctcagctgcagcctccccattcc -858

**FIG. 7B**

```
-857  ctggggcctgccacgccctccactgcctcaaggatgcgtctgagcctggcctgcacatcc  -798

-797  atgctcccaccggctggaggggtgttctggggccctgggggaccgtatatctggggagg  -738

-737  gggagggatccgccctaggggtgctgtgtggtgccccatagccaggcaagtctgaggtgg  -678

-677  acggcccgtcctcgccttgtgagcgaggcagagctgagctgagctgcccctcctgcctaa  -618

-617  cacgccactgtctctggagatcgggctgtgcgtgaacatgcggagcctgccctggtacgt  -558

-557  cccggccaaccccgactccttcttcccacgctgctacagcctctgcaccgagagtgagca  -498

-497  gcaggagttcctgggtaagtgaggagacggcagagggccccagtgctgtcagcagagagg  -438

-437  cttctagaaagatccccctggtgctgagacagactgatggggcagggtctgaggatagag  -378

-377  gaccggggagaggcctcccatggtcatggtcatggcagtacagaggccaggggccccggg  -318

-317  agggagggcgggcagtcaaggagtgtgtggttctgtgctaggcttgtggacagcgcggcg  -258

-257  agcagctggggcaaggccggctccgtggtcggaggccgaggggtgcagctggacggccgc  -198

-197  agtcacagagacactgcagggagaagggcaggcagactgggggtgtgggagcaggcctgg  -138

-137  gccccatcggctatgagggcgggaagtggggcgggttggggagcctccgtggccctggcc   -78

 -77  ccatctccagtccccagtcctggctcggacagatagggcgaggctgtgctgtcctttcag   -18

 -17  aagacttccggcgcaccatggcatccagcatcctcaagtgggtggtcagccaccagagct    42
   1                  M  A  S  S  I  L  K  W  V  V  S  H  Q  S  C    15

  43  gcagcaggagcagcagaagcaagcccagggaccagagggaggaggccgggagcagcgacc   102
  16    S  R  S  S  R  S  K  P  R  D  Q  R  E  E  A  G  S  S  D  L    35

 103  tgagcagcaggcaaggtgcgctgggccggggcagggcagtgccaggccaccagagctcgg   162
  36    S  S  R  Q  G  A  L  G  R  G  R  A  V  P  G  H  Q  S  S  G    55

 163  ggcctccacaggggccctccc  183
  56    P  P  Q  G  P  S     61
```

FIG. 8

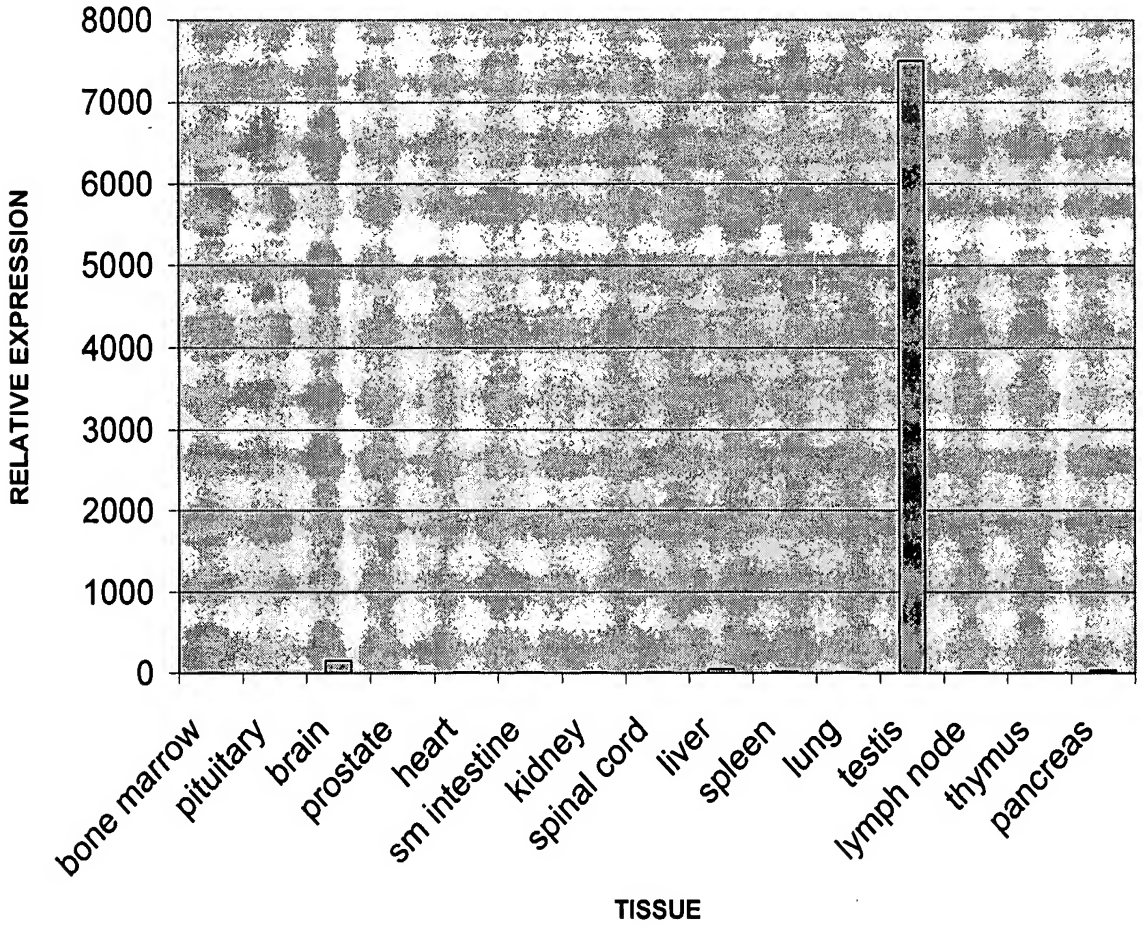
8000
7000
6000
5000
4000
3000
2000
1000
0
RELATIVE EXPRESSION
bone marrow
pituitary
brain
prostate
heart
sm intestine
kidney
spinal cord
liver
spleen
lung
testis
lymph node
thymus
pancreas
TISSUE

FIG. 9

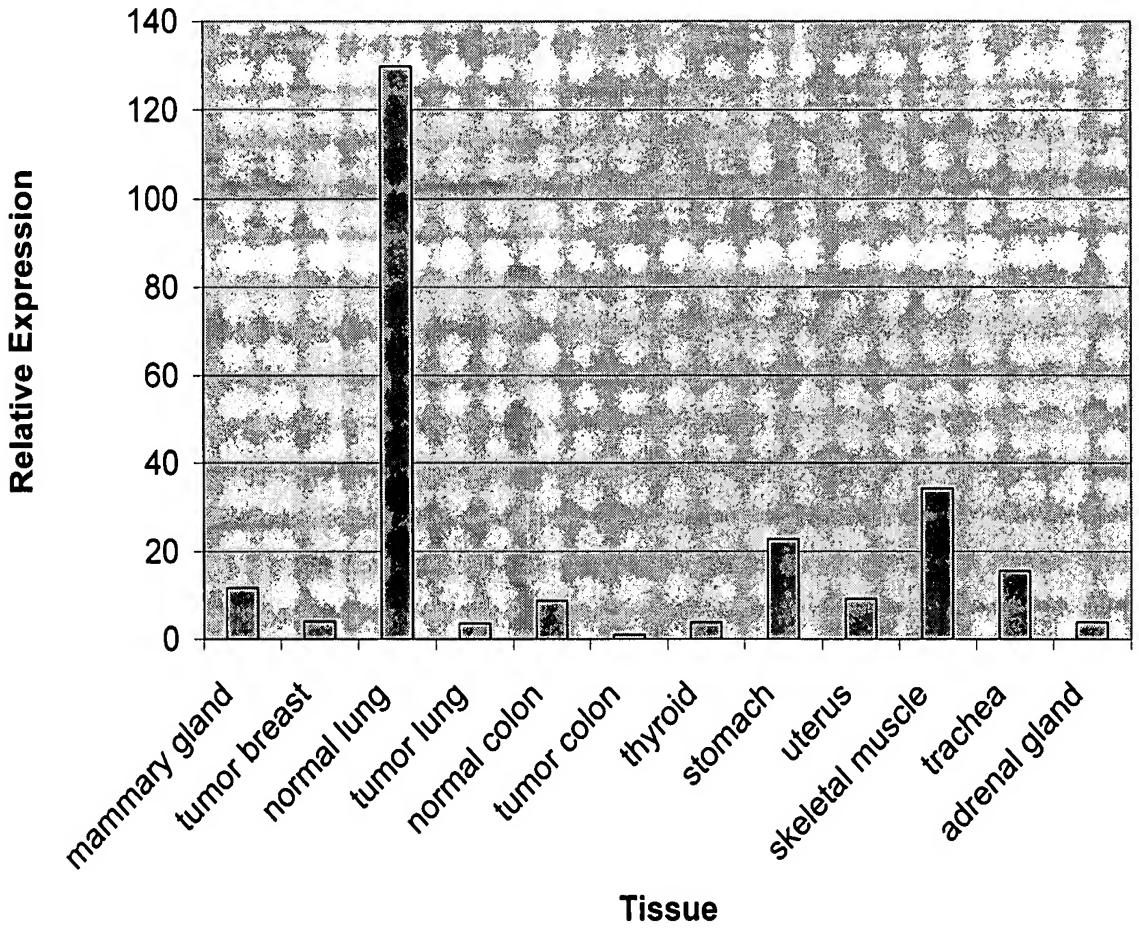
Relative Expression
140
120
100
80
60
40
20
0
mammary gland
tumor breast
normal lung
tumor lung
normal colon
tumor colon
thyroid
stomach
uterus
skeletal muscle
trachea
adrenal gland
Tissue

**FIG. 10**

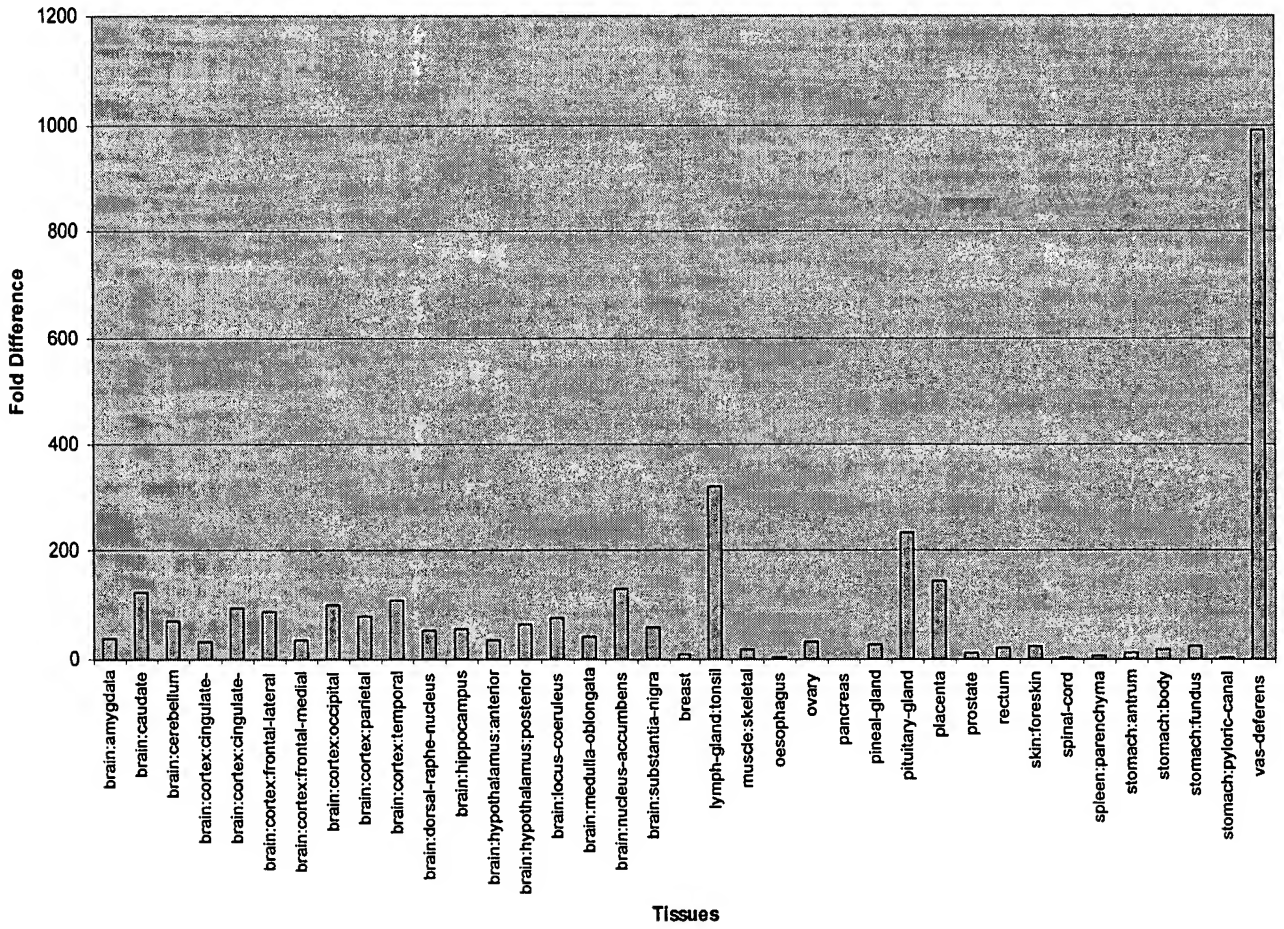
Fold Difference
1200
1000
800
600
400
200
0
brain:amygdala
brain:caudate
brain:cerebellum
brain:cortex:cingulate-
brain:cortex:cingulate-
brain:cortex:frontal-lateral
brain:cortex:frontal-medial
brain:cortex:occipital
brain:cortex:parietal
brain:cortex:temporal
brain:dorsal-raphe-nucleus
brain:hippocampus
brain:hypothalamus:anterior
brain:hypothalamus:posterior
brain:locus-coeruleus
brain:medulla-oblongata
brain:nucleus-accumbens
brain:substantia-nigra
breast
lymph-gland:tonsil
muscle:skeletal
oesophagus
ovary
pancreas
pineal-gland
pituitary-gland
placenta
prostate
rectum
skin:foreskin
spinal-cord
spleen:parenchyma
stomach:antrum
stomach:body
stomach:fundus
stomach:pyloric-canal
vas-deferens
Tissues

**FIG. 11**

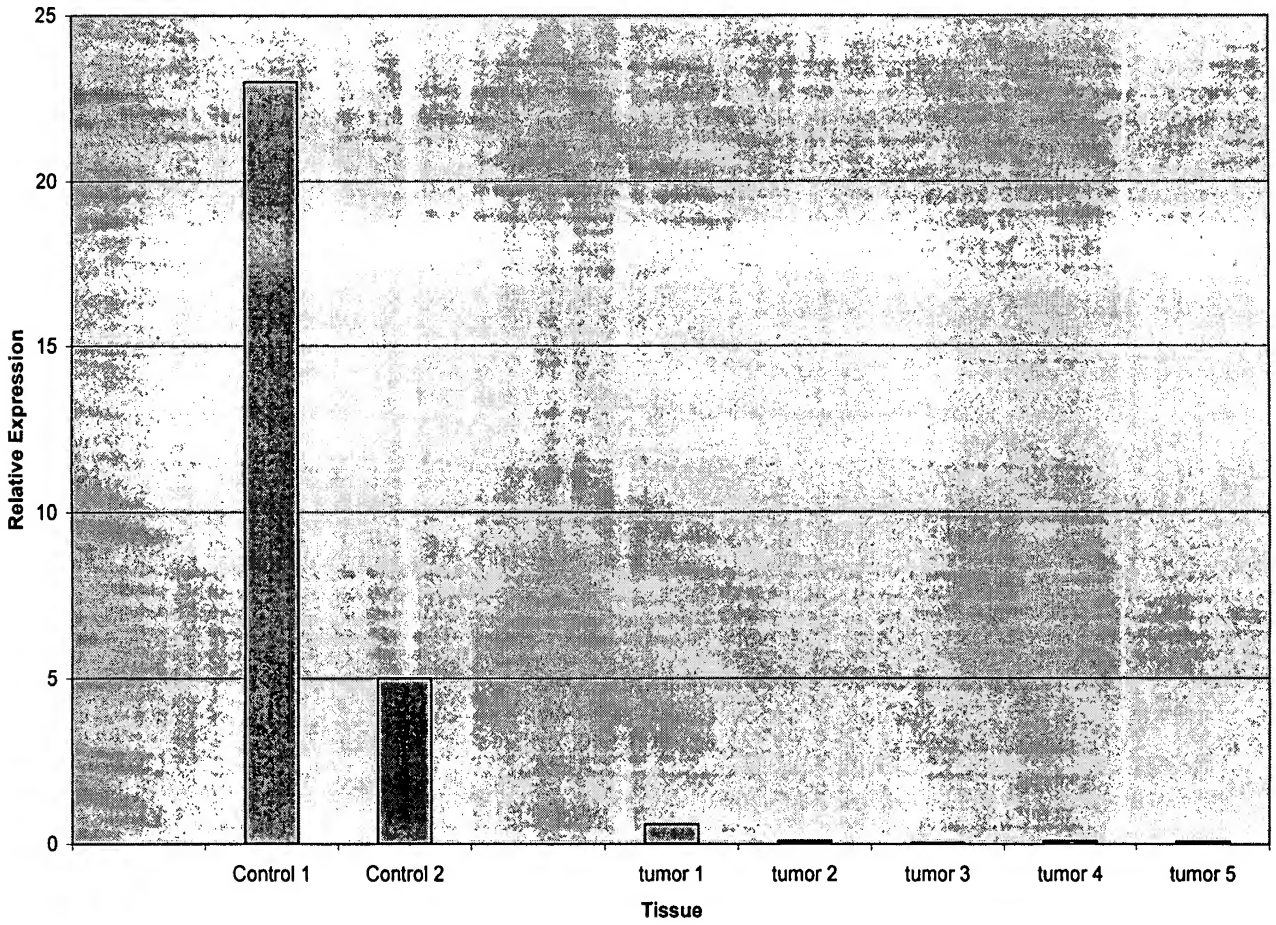
25
20
15
10
5
0
Relative Expression
Control 1
Control 2
tumor 1
tumor 2
tumor 3
tumor 4
tumor 5
Tissue

**FIG. 12**

| Protein | Genbank ID | Identities | Similarities |
|---|---|---|---|
| Human HOTTL protein | gi\|6683745 | 57.5% | 65.5% |
| Pig tubulin--tyrosine ligase protein (TTL) | gi\|423218 | 29.4% | 40.0% |
| Human tubulin tyrosine ligase-like protein (TTLH_HUMAN) | gi\|20455371 | 53.3% | 61.4% |
| Human tubulin tyrosine ligase-like protein (TTLL_HUMAN) | gi\|20455347 | 27.4% | 38.4% |

FIG. 13

```
1gsaA   MIKLGIVMDP IANINIKKDS SFAMLLEAQR RGYELHYMEM GDLYLINGEA
BGS42   .......... .......MAS SILKWVVSHQ SCSRSSRSKP RDQREEAGSS

1gsaA   RAHTRTLNVK QNYEEWFSFV GEQDLPLADL DVILMRKDPP FDTEFIYATY
BGS42   DLSSRQDA.. ENAEAKLRGL PGQLVDIACK VCQAYLGQLE HEDIDTSADA

1gsaA   ILERAEEKGT LIVNKPQSLR DCNEKLFTAW FSDLTPETLV TRNKAQLKAF
BGS42   VEDLTEAEWE DLTQQYYSLV HGDAFISNSR NYFSQCQALL NRITSVNPQT

                ^* ^*      *   *                            ^^*
1gsaA   WEKHS..DII LKPLDGMGGA SIFRVKEGDP NLGVIAETLT EHGTRYCMAQ
BGS42   DIDGLRNIWI IKPAAKSRGR DIVCMDRVEE ILELAAADHP LSRDNKWVVQ
         **            *    ^ ^
1gsaA   NYLPAIKDG. ....DKRVLV VDGEPVPYCL ARIP...... ..........
BGS42   KYIETPLLIC DTKFDIRQWF LVTDWNPLTI WFYKESYLRF STQRFSLDKL

1gsaA   .......... .......... .......... .QGGETRGNL AAGGRGEPRP
BGS42   DSAIHLCNNA VQKYLKNDVG RSPLLPAHNM WTSTRFQEYL QRQGRGAVWG

                                        ^         *^^ ^*      ^*
1gsaA   L......... ..TESDWKIA RQIGPTLKEK GLIFVGLDII GDR.....LT
BGS42   SVIYPSMKKA IAHAMKVAQD HVEPRKNSFE LYGA...DFV LGRDFRPWLI

        *^*
1gsaA   EINVTSPTCI REIEAEFPVS ITGMLMDAIE ARLQ...... ..........
BGS42   EINSSPTMHP STPVTAQLCA QVQEDTIKV. AVDRSCDIGN FELLWRQPVV

1gsaA   .......... .......... .......... .......... ..........
BGS42   EPPPFSGSDL CVAGVSVRRA RRQVLPVCNL KASASLLDAQ PLKARGPSAM

1gsaA   .......... .......... .......... .......... ..........
BGS42   PDPAQGPPSP ALQRDLGLKE EKGLPLALLA PLRGAAESGG AAQPTRTKAA

1gsaA   .......... .......... .......... .......... ..........
BGS42   GKVELPACPC RHVDSQAPNT GVPVAQPAKS WDPNQLNAHP LEPVLRGLKT

1gsaA   .......... .........
BGS42   AEGALRPPPG GKGS.....
```
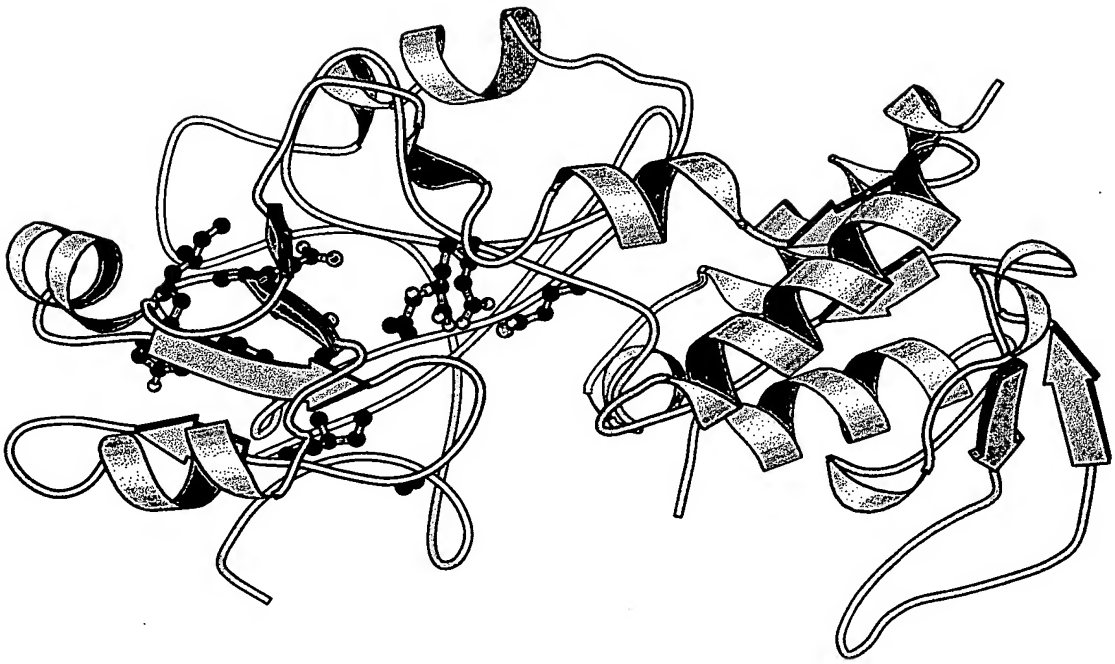
FIG. 14